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Effect of pulse and continuous addition of oleate on microbial communities involved in anaerobic digestion process

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Abstract

Oleic acid is the most abundant long chain fatty acid (LCFA) present in industrial and domestic wastewaters. However there is still a lack of knowledge regarding the microbiological aspects of the complex consortia involved in LCFA degradation during anaerobic digestion of high strength wastewaters. The aim of the present work was to evaluate microbial diversity of bacteria and archae in anaerobic reactors treating cattle manure during continuous addition, CA ($2\text{g oleate}\cdot\text{L}^{-1}\cdot\text{day}^{-1}$) and pulse addition, PA of oleate (final concentration $5\text{g}\cdot\text{L}^{-1}$) under thermophilic methanogenic conditions. Non exposed to LCFA thermophilic digested manure from a full scale biogas plant (Vegger, Denmark) was used as inoculum. PCR-DGGE combined with sequence and phylogenetic analysis was used to study bacterial and archaeal community changes and identify the microorganisms involved in oleate degradation. Results obtained showed significant shift in bacterial community structure which was more pronounced during CA of oleate. Similar trend was also observed for archaeal communities but changes were less remarkable indicating that dominant archaeal composition remained relatively stable over operation. Bacterial and archaeal similarity indices between reactor effluents and original inoculum decreased up to 60.2 and 65.9 respectively in the reactor with CA compared to 84.7 and 88.4 in the reactor with PA. Bacterial community changes in response to LCFA addition resulted in a new and less diverse bacterial consortium related to functional specialization towards LCFA degradation. For the archaeal domain, the sequences were affiliated within *Euryarchaeota* phylum. Results obtained in this study delivered a detailed comprehensive picture on LCFA degrading microbial communities in high organic strength wastewater such as animal manure.